

Figure 1.

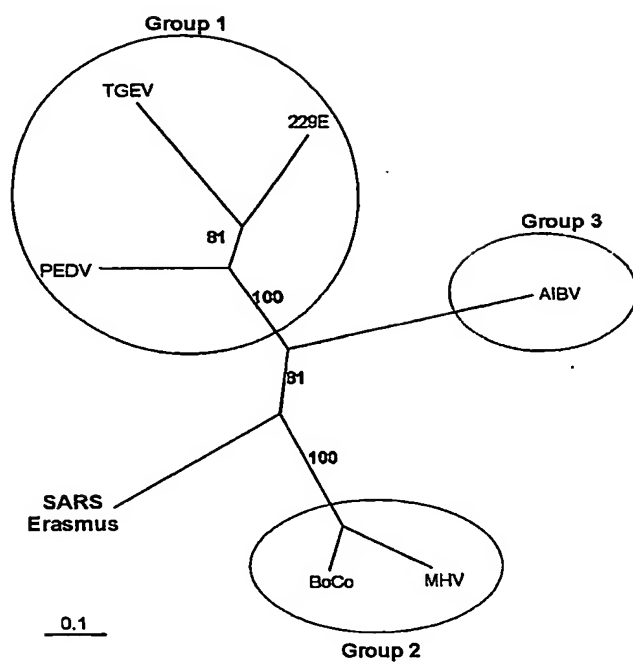


Figure 2 RNA sequences, implied polypeptides and alignment with one close relative

EMC-1

5 UUGUAAACUGGUGGUCUUGUACAACAGACUUCUCAGUGGUUGUCUAAUCUUUUGGGCACUACUGGUUGAAAAAC
 UCAGGCCUAUCUUUGAAUGGAUUGAGGCGAAACUUAGUGCAGGAGUUGAAUUUCUCAAGGAUGCUUGGGAGAU
 UCUCAAAUUUCUCAUUACAGGUGUUUUUGACAUCGUCUACAGGGUCAAAUACAGGUUGCUUCAGAUAAACAUCAAG
 GAUUGUGUAAAUGCUUCAUUGAUGUUGUUAACAAGGCACUCGAAUUGUGCAUUGAUCAAGUCACUAUCGCUG
 GCGCAAAGUUGCGAUCACUACAACUAGGUAAGUCUUCUACGCUCAAAGCAAGGGACUUUACCGUCAGUGUAU
 10 ACGUGGCAAGGAGCAGCUGCAACUACUAGCUGCCUCUUAAGGCACCAAAAGAAGUAACCUUUCU
 UGAAGGUGAUUCACAUGACACAGUACUUAACCUCUGAGGAGGUUGUUCUCAAGAACGGUGAA
 CUCGAAGCACUCGAGACGCCCUGUAGAUAGCUUCACAAAUGGAGCUAUCGUUGGCACACCAG
 UCUGUGUAAAUGGCCUCAUGCUCUUAAGAGAUUAAGGACAAAGAACAUAUCUGCGCAUUGUC
 UCCUGGUUUACUGGCUACAAACAAUGUCUUAUCGCUUAAAAGGGGGUGCACCAAUUAAAGGU
 15 GUAACCUUUGGAGAAGAUACUGUUUGGGAAGUUCAGGGUUAACAAGAAUGUGAGAAUCACAU
 UUGAGCUUGAUGAACGUGUUGACAAAGUGCUUAAUGAAAAGUGCUCUGUCUACACUGUUGA
 AUCCGGUACCGAAGUACUGAGUUUGCAUGUGUUGUAGCAGAGGCUGUUGUGAAGACUUUA
 CAACCAGUUUCUGAUC

20 **Translation** Nucleotides 7 to 870: Frame 1; 288 aa

LVLVLYNRLLSGCLIFWALLVEKLRPIFEWIEAKLSAGVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVCFIDV
 NKALEMCIDQVTIAGAKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPKAPKEVTFLEGDSHDTVLTSEEVVLKNGEL
 EALETVPDSFTNGAIVGTPVCVNLMLLEIKDKEQYCALSPGLLATNNVFRKGGAPIKGVTFGEDTVWEVQGYKNVRITF
 ELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLQPVSD

25 **Alignment**

RNA-directed RNA polymerase (orfla) murine hepatitis virus
 Identities = 72/285 (25%), Positives = 118/285 (41%)

30 Query: 49 FWALLVEKLRPIFEWIEAKLSAGVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCV 228
 F AL V +R I EW + L+ + W + L+ G+F + G I + + + V
 Sbjct: 638 FKALGVAVVRKITEWFD--LAVDIAASAAGWLCYQ-LVNGLFAVANGVITFVQE-VPELV 693

35 Query: 229 KCFIDVVKALEMCIDQVTIA---GAKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMP 399
 K F+D ++ ID +++ G + V +A SK +Y + K +MP
 Sbjct: 694 KNFVDKFKAFFKVLIDMSVSILSGLTVVKTASNRVCLAGSK-VYE--VVQKSLSAYVMP 750

40 Query: 400 LKAPKEVTFLEGDSHDTVLTSEEVVLKNGEL--EALETVPDSFTNGAIVGTPVCVNLML 573
 + E T L G+ V + V + L + P SF IV L
 Sbjct: 751 VGC-SEATCLVGEIEPAVFEDDVVDVVKAPLTYQGCKPPTSFEKICIVDK-----L 801

45 Query: 574 LEIKDKEQYCAL-----SPGLLATNNVFRKGGAPIKGVTFGEDT-VWEVQGYKNVRITF 735
 K +Q+ + + G+L F G K V F + V ++ + ++ITF
 Sbjct: 802 YMAKCGDQFYFVVVDNDTVGVLDQCWRFPFCAG----KKVEFNDKPKVRKIPSTRKIKITF 857

50 Query: 736 ELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLQPVSD 870
 LD D VL++ CS + V+ + E VV +AV TL P +
 Sbjct: 858 ALDATFDSVLSKACSEFEVDKDVTLDELDDVVLDAVESTLSPCKE 902

EMC-14

CAUCCAGCUUCUUAAGGCAGCAUAUGAAAAUUUCAAUUCACAGGACAUCUUAUUGCACCAUUGUUGUCAGCA
 GGCAUAUUUGGUGCUAAACCACUUCAGUCUUUACAAGUGUGCGUGCAGACGGUUCGUACACAGGUUUUAUUG
 CAGUCAUAGACAAAGCUCUUUAUGAGCAGGUUGUCAUGGAUUAUCUUGAUAAACCUGAAGCCUAGAGUGGAAGC
 55 ACCUAAACAAGAGGAGCCACCAAACACAGAAGAUUCCAAAACUGAGGAGAAAUCUGUCGUACAGAAGCCUGUC
 GAUGUGAAGCCAAAAAUUAAGGCCUGCAUUGAUGAGGUUACCACAACACUGGAAGAAACUAAGUUUCUUACCA
 AUAAGUUACUCUUGUUGCUGAUUAUCAAUGGUAAGCUUUACCAUGAUUCUCAGAACAUAGCUUAGAGGUGAAGA
 UAUGUCUUUCCUUGAGAAGGAUGCACCUCUACAUGGUAGGUGAUGUUUAUCACUAGUGGUGAUUAUCACUUGUGUU

Fig. 2 Cont.

GUAAUACCCUCCAAAAAGGCUGGUGGCACUACUGAGAUGCUCUCAAGAGCUUUGAAGAAAGUGCCAGUUGAUG
AGUAUAUAACCACGUACCCUGGACAAGGAUGUGCUGGUUAUACACUUGAGGAAGCUAAGACUGCUCUUAAGAA
AUGCAAUUCUGCAUUUUUAUGUACUACCUUCAGAAGCACCUAUUGCUAAGGAAGAGAUUCUAGGAACUGUAUCC
UGGAAUUGAG

Translation

Nucleotides 5 to 739: Frame 2; 245 aa

IQLLKAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQVYIAVNDKALYEQVMDYLDNLKPRVEAPKQEEPPN
TEDSKTEEKSVVQKPVVDVKPKIKACIDEVTTTLEETKFLTNKLLLFADINGKLYHDSQNMLRGEDMSFLEKDAPYMGVDVI
TSGDITCVVIPSCKKAGGTTEMLSRALKKVPVDEYITTPGQGCAGYTLLEEAKTALKKCKSAFYVLPSEAPNAKEEILGTVS
WN

Alignment

replicase polyprotein lab Human coronavirus 229E

Identities = 48/202 (23%), Positives = 83/202 (41%), Gaps = 13/202 (6%)
Frame = +2

Query: 8 LLKAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRT---QVYIAVNDKALYEQV 178
L+KA N Q L P+LS GIFG K SL+V + T +V++ + + +
Sbjct: 1371 LIKAYNTINNEQGTPLTPILSCGIFGIKLETSLEVLLDVCNTKEVKVFVYTDTEVCKVKD 1430

Query: 179 VMDYLDNLKPRVEAPKQEEPPNTEDSKTEEKSVVQKPVVDVKPKIKACIDEVTTTLEETKF 358
+ L N++ +VE PK E P V KP V K +++ ++
Sbjct: 1431 FVSGLVNVQ-KVEQPKIEPKP-----VSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPI 1483

Query: 359 L--TNKLLLFADINGKLYHDSQNMLRG--EDMSFLEKDAP-----YMGVDVITSGDITC 508
+ T+ +L D L + +L +D + K P + +G V+ +
Sbjct: 1484 VLFTDSMLTLDDRGLALDNLASGVLSAAIKDCVDINKAIPSGNLIKFDIGSVV----VYM 1539

Query: 509 VVIPSCKKAGGTTEMLSRALKKV 574
V+PS+K + R +K+
Sbjct: 1540 CVVPSEKDKHLDNNVQRCTRKL 1561

EMC-2

UCGAGAUUUcAUcUUGACGGUGCAGGUUCUUUCACUUGACAAACUAAAGAGUCUCUUAUCCCCUGCGGGAGGUU
AAGACUAUAAAAGUGUUCACAACUGUGGACAACACUAAUCUCCACACACAGCUUGUGGAUAUGUCUAUGACAU
AUGGACAGCAGUUUGGUCCAACAUACUUGGAUGGUGCUGAUGUUACAAAAUUAACCUCUAUGUAAAUCAUGA
GGGUAAGACUUUCUUUGUACUACCUAGUGAUGACACACUACGUAGUGAAGCUUUCGAGUACUACCAUACUCUU
GAUGAGAGUUUUUCUUGGUAGGUACAUGUCUGCUUUAACCACACAAAGAAAUGGAAA

Translation

Nucleotide 2 to 349: Frame 2; 116 aa

RDFILTVQVLSLDKLSLLSLREVKTIKVFTTVDNTNLHTQLVDMSMTYGQQFGPTYLDGADVTKIKPHVNHEGKTFVFLP
SDDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWK

Alignment

> Bovine Coronavirus RNA-Dependent RNA polymerase

Identities = 25/90 (27%), Positives = 44/90 (48%)
Frame = +2

Query: 80 IKVFTTVDNTNLHTQLVDMSMTYGQQFGPTYLDGADVTKIKPHVNHEGKTFVFLPSDDL 259
+ + TVD N + V + ++G+ G + DG +VTK K +N++GK FF + +
Sbjct: 1565 VDILLTVDGVNFTNRFVPVGESEFGKSLGNVFCGYNVTKHKCDINYGKGVFFQFDNLSSE 1624

Query: 260 RSEAFEYYHTLDESFLGRYMSALNHTKKWK 349
+A D+ L Y + L + KW+
Sbjct: 1625 DLKAVRSSFNFDQKELLAYYNMLVNCSEKWK 1654

Fig. 2 Cont.

EMC13:

CUGAAGAAGUAGUGGaAAAUCCUACCAUACAGAAGGAAGUCAUAGAGUGUGACGUGAAAACUACCGAAGUUGU
 AGGCAAUGUCAUACUUAACCAUCAGAUGAAGGUGUUAAGUAACACAAGAGUUAGGUCAUGAGGAUCUUAUG
 GCUGCUUAUGUGGAAAACACAAGCAUUAACCAUUAAGAAACCUAUAGAGCUUUCACUAGCCUUAAGGUUUAAAAA
 5 CAAUUGCCACUCAUGGUUAUUGCUGCAAUUAAUAGUGUCCUUGGAGUAAAAUUUUGGCUUAUGUCAAAACCAU
 CUUAGGACAAGCAGCAAUUACAACAUCAAAUUGCGCUAAGAGAUUAGCACAACGUGUGUUUAACAAUUAUAG
 CCUUAUGUGUUUACAUUAUUGUUCCAAUUGUGUACUUUUACUAAAAGUACCAUUCUAGAAUUAAGAGCUUCAC
 UACCUACAACUAUUGCUAAAAAUAGUGUUAAGAGUGUUGCUAAAAUUAUGUUUGGAUGCCGGCAUUAUUAUAGU
 10 GAAGUCACCCAAAUUUUCUAAAUUGUUCACAAUCGCUAUGUGGCUAUUGUUGUUAAGUAUUUGCUUAGGUUCU
 CUAAUCUGUGUAAUCUGCUGCUUUUGGUGUACUCUUAUCUAAUUUUGGUGCUCCUUCUUAUUGUAAUGGCGUUA
 GAGAAUUGUAUCUUAUUCGUCUACGUGUACUACUAGGAUUUCUGUGAAGGUUCUUUUCCUUGCAGCAUUG
 UUUAAUGUGGAUUAAGACUCCCUUGAUUCUUAUCCAGCUCUUGAAACCAUUCAGGUGACGAUUUCAUCGUACAAG
 CUAGACUUGACAAUUUUAGGUCUGGCCGCGUG

Translation

>-out: 3 to 833; Frame 3 277 aa

EEVVENPTIQKEVIECDVKTTEVVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIATHGIAA
 INSVPSKILAYVKPFLGQAAITTSNCAKRLAQRVFNNYMPYVFTLLFQLCTFTKSTNSRIRASLPTTIKNSVKSVAKLC
 20 LDAGINIVKSPKFSKLFITIAMWLLLLSICLSGLICVTAAFGVLLSNFGAPSYCNGVRELYLNSSNVTMTDFCEGSFPCISIC
 LSGLDSDLSYPALETIQVTISSYKLDLTILGLAA

Alignment

bovine coronavirus RNA-dependent RNA Polymerase

Identities = 50/269 (18%),

25 Query: 57 KTTEVVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIATH- 233
 K +V +VI+ +K + L D+ ++ ++ N+LS+A+ + TI
 Sbjct: 2046 KPEKVEDSVIVNDDTSEIKYVKSLSIVDVYDMWLTGCRYVVRTANDLSMAVNVPTIRKFI 2105

30 Query: 234 --GIAAINSVPWSKI-LAYVKPFLGQAAITTSNCAKRLAQRVFN--NYMPYVFTLLF--- 389
 G+ + S+P + L +KP N K + ++ N++ ++F LLF
 Sbjct: 2106 KFGMTLV-SIPIDLLNLRKIPVF-----NVVKAVRNKISACFNFIKWLFVLLFGWI 2156

35 Query: 390 -----QLCTFTKSTNSRIRASLPTTIKNSVKSVAKLCLDAGINIVKSPKFSKLFITIAMW 554
 +T S++ L KN+ + + G + + +W
 Sbjct: 2157 KISADNKVIYTTEVASKLTCKLVALAKNAFLTFKWSVVARGACIIAT-----IFLLW 2209

Query: 555 XXXXXXXXXXXXXVTAAFGVLLSNFGAPSYCNGVRELYLNSSNVTM----- 695
 G L P++ + + ++ ++ T+
 40 Sbjct: 2210 FNFIYANVIFSDFYLPKIGFL-----PTFVGKIAQWIKSTFSLVTICDLYSIQDVGFKN 2263

Query: 696 DFCEGSFPCISICLSGLDSDLSYPALETIQ 782
 +C GS C CL+G D LD+Y A++ +Q
 Sbjct: 2264 QYCNGSIACQFCLAGFMDLDNYKAIDVVQ 2292

EMC-3

GUGGUAAGAUUGUUAGUACUUGUUUUAACUUAUGCUUAAGGCCACAUUAUUGUGCGUUCU
 UGCUGCAUUAUGUUUGUUAUUCGUUAUGCCAGUACAUUAUGUCAUCCAUGAUGGUUAC
 ACAAAUGAAAUCAUUGGUUACAAAGCCAUUCAGGAUGGUGUCACUCGUGACAUCAUUUCUA
 50 CUGAUGAUUGUUUGCAAUUAACAUGCUGGUUUUGACGCAUGGUUUAGCCAGCGUGGUGG
 UUCAUACAAAAUGACAAAAGCUGCCCUGUAGUAGCUGCUAUCAUUACAAGAGAGAUUGGU
 UUCAUAGUGCCUGGCUUACCGGGUACUGUGCUGAGAGCAAUCAUUGGUGACUUCUUGCAU
 UCCUACCUCGUGUUUUUAGUGCUGUUGGCAACAUUGCUACACACCUUCCAACUCAUUGA
 GUUAUGUGAUUUUGCUACCUCU

Translation

Nucleotide 3-449; 149 aa

GKIVSTCFKMLKATILLCVLAALVCYIVMPVHTLSIHGYTNEIIGYKAIQDGVTRDIIISTDDCFANKHAGFD
 AWFSQRGGSYKNDKSCPVVAIIITREIGFIVPGLPGTVLRAINGDFLHFLPRVFSAVGNICYTPSKLIEYSDF
 60 ATS

Fig. 2. Cont.

Alignment

> Murine Hepatitis Virus RNA-Dependent RNA polymerase

5 Identities = 48/126 (38%),

Query: 78 YIVMPVHTLSIHGTYTNEIIGYKAIQDGVTRDIISTDDCFANKHAGFDWFSQRRG--SY 251
 + +MP + + D +K I +GV RD+ TD CFANK FD W+ G Y
 Sbjct: 2859 WALMPTYAVHKSMDQLPLYASFVIDNGVLRDVSVDACFANKFNQFDQWYESTFGLAYY 2918

10 Query: 252 KNDKSCFVVAIIITREIGFIVPGLPGTVLRAINGDFLHFLPRVFSAVGNICYTPSKLIEY 431
 +N K+CPVV A+I ++IG + +P TVLR LHF+ F+ CYTP I Y
 Sbjct: 2919 RNSKACPVVVAVIDQDIGHTLNFVPTTVLR-YGFHVLHFITHAFATDSVQCYTPHMQIPY 2977

15 Query: 432 SDFATS 449
 +F S
 Sbjct: 2978 DNFYAS 2983

EMC-4

20 ACAGACAUCAAUCACUUCUGCUGUUCUGCAGAGUGGUUUUAGGAAAAUGGCAUUCCCGUCAGGCAAAGUUGAA
 GGGUGCAUGGUACAAGUAACCUGUGGAACUACAACUCUUAUUGGAUUGUGGUUGGAUGACACAGUAUACUGUC
 CAAGACAUGUCAUUUGCACAGCAGAAGACAUGCUUAAUCCUAACUAUGAAGAUUCUGCUCAUUCGCAAUCCAA
 CCAUAGCUUUUCUUGUUCAGGCUGGCAAGUUAACUUCGUGUUAUUGGCCAUUCUAUGCAAAAUUGUCUGCUU
 AGGCUUAAAGUUGAUACUUCUAACCCUAAGACACCCAAGUAUAAAUUUGUCCGUAUCCAACCGGUAACAAU
 25 UUCAGUUCUAGCAUGCUACAAGGUUCACCAUCUGGUGUUUAUCAGUGUGCCAUGAGACCUAUUAUACCAU
 UAAAGGUUCUUAUUGGAUCAUGUGGUAGUGUUGGUUUUAACAUUGAUUAUGAUUGCGUGUCUUCUGC
 UAUUAGCAUCAUUGGAGCUUCCAACAGGAGUACACGCUGGUACUGACUAGAAGGUAAAUUCUAUGGUCCAU
 UUGUUGACAGACAAACUGCACAGGCUGCAGGUACAGACACAACCAUAAAUUGUUUUGGCAUGGCUGUA
 UGCUGCUGUUAUCAUGGUGUAU

Translation

Nucleotides 2 to 679: Frame 2; 226 aa

QTSITSAVLQSGFRKMAFSPGKVEGCMVQVTCGTTTLNGLWLDLTVYCPRHVICTAEDMLNPYEDLLIRKSNHSLVQAG
 NVQLRVIGHSMQNCLLRLKVDTSNPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMPNHTIKGSFLNGSCGSVGFNI
 35 DYDCVSFCYMHMELPTGVHAGTDLEGKFYGFVDRQTAQAAGTDTTITLNVLAWLAAVINGD

Alignment

RNA-directed RNA polymerase murine hepatitis virus

40 Identities = 122/222 (54%)

Query: 8 SITSAVLQSGFRKMAFSPGKVEGCMVQVTCGTTTLNGLWLDLTVYCPRHVICTAEDMLNP 187
 S+T++ LQSG KM P+ KVE C+V VT G TLNGLWLDL TVCPRHVIC++ DM +P
 45 Sbjct: 3326 SVTTSFLQSGIVKMSPTSKEPCIVSVTYGNMTLNLGLWLDLTVYCPRHVICSSADMTDP 3385

Query: 188 NYEDLLIRKSNHSLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPKTPKYKFVRIQPGQTF 367
 +Y +LL R ++ F V +G + L V+ + MQ C L L V NP TPKY F ++PG+TF
 50 Sbjct: 3386 DYPNLLCRVTSSDFCVMSGRMSLTVMYSQMQCQLVLTTLQNPNTPKYSFGVVKPGETF 3445

Query: 368 SVLACYNGSPSGVYQCAMPNHTIKGSFLNGSCGSVGFNIDYDCVSFCYMHMELPTGVH 547
 +VLA YNG P G + +R +HTIKGSFL GSCGSVG+ + D V F YMH +EL TG H
 55 Sbjct: 3446 TVLAAYNRPQGAHFVTLRSSHTIKGSFLCGSCGSVGVLTDGDSVRFVYMHQLELSTGCH 3505

Query: 548 AGTDLEGKFYGFVDRQTAQAAGTDTTITLNVLAWLAAVIN 673
 GTD G FYGP+ D Q Q D T T+NV+AWLYAA+ N
 Sbjct: 3506 TGTDFSGNFYGPYRDAQVVLQFVDYQTQTVNVVAWLAAIFN 3547

EMC-5

60 Note that this sequence is not fully in frame.

AGUUGGAAAAGAUGGCAGAUACAGGCUAUGACCCAAAUGUACAAACAGGCAAGAUCUGAGGA
 CAAGAGGGCAAAGUAACUAGUGCUAUGCAAACAAUGCUCUUCACUAUGCUUAGGAAGCUU
 GAUAAUGAUGCACUUAACAACAUAUAACAUAUGCGCGUGAUGGUUGUGUCCACUCAACA
 UCAUACCAUUGACUACAGCAGCCAAACUAUGGUUGUUGUCCUGAUUAUGGUACCUACAA
 65 GAACACUUGUGAUGGUAACACCUUUACAUAUGCAUCUGCACUCUGGGAAAUCCAGCAAGUU
 GUUGAUGCGGAUAGCAAGAUUGUUAACUUAUGUGAAAUAACAUGGACAAUUCACCAAU
 UGGCUUGGCCCCUUAUUGUUAACAGCUCUAAGAGCCAAACUCAGCUGUUAACUACAGAAUAA
 UGAACUGAGUCCAGUAGCACUACGACAGAUGUCCUGUGCGGCUGGUACCAACACAAACAGCU
 UGUACUGAUGACAAUGCACUUGCCUACUAUAACAUAUUCGAAGGGAGGUAGGUUUGUGCUGG

Fig. 2. Cont.

CAUUACUAUCAGACCACCAAGAUCUCAAAUGGGCUAGAUUCCCUAAGAGUGAUGGUACAGG
 UACAAUUUACACAGAACUGGAACCACCUUGUAGGUUUGUACAGACACACCAAAGGGCCU
 AAAGUGAAAUACUUGUACUUAUCAAGGCUUAAACAACCUAAAUAAGAGGUAUGGUGCUGGG
 CAGUUUAGCUGCUACAGUACGUCUUCAGGCUGGAAAUGCUACAGAAGUaCCUGCCAAUUA
 5 ACUGUGCUUUCCUUCUGUGCUUUUGCAGUAGACCCUGCUAAAAGCAUAUaAAGGAUUACCUA
 GCAAGUGGAGGACAACCAAUACCAACUGUGUGAAGAUGUUGUGUACACACACUGGUACAG
 GACAGGCAAUUACUGUAACACCAGAAGCUAACAUGGACCAAGAGUCCUYUGGUGGUGCUUC
 AUGUUGUCUGUAUUGUAGAUGCCCAUUGACCAUCCAAAUCCUAAAGGAYUCUGUGACUUG
 AAAGGUAAGUACGUCCAAAUACCUACCACUUGUGCUAAUGACCCAGUGGGUUUUACACUUA
 10 GAAACACAGUCUGUACCGUCUGCGGAAUGUGGAAAGGUUAUGGCUGUAGUUGUGACCAACU
 CCGCGAACCUCUAGUCAGUCUGCGGAUGCAUCAMCGUUUUUAAACGGGUUUGCGGUGUAA
 GUGGACCCGUCUUAACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUCUACAGGGCUUU
 UGAUAUUUACAACGAAAAGUUGCUGGUUYUGCAAAGUUCUAAAAACUAA

Translation 1

Nucleotide 3-701 ; 233 aa

LEKMADQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRKLNDNDALNNIINNARDGCVPLNIIPLTTAAKLMVV
 VPDYGTYNKTCDGNTFTYASALWEIQVVDADSKIVQLSEINMDNSPNLAWPLIVTALRANSVAVKLQNNELSP
 VALRQMSCAAGTTQTACTDDNALAYNNNSKGGRFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTD
 20 PKGPKVKYLYFIKA

Translation 2

FKRVCVSA-ARLTFCGTGTSTDVVYRAFDIYNEKVAGXAKFLK

Alignment 1 of translation 1 sequence

RNA-Dependent RNA Polymerase: bovine coronavirus
 Identities = 181/413 (43%),

Query: 3 LEKMADQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRXXXXXXXXXXXXXXXXXRDGCVPLN 182
 LE+MAD A+T MYK+AR DK++KV SA+QTMFL+M+RK GCVPLN
 30 Sbjct: 3985 LERMADLALTNMYKEARINDKRSKVVSALQTMFLSMVRKLDNQALNSILDNAVKGCVPLN 4044
 Query: 183 IIPLTAAKLMVVVPDYGTYNKTCDGNTFTYASALWEIQVVDADSKIVQLSEINMDNSP 362
 IP A L ++VPD Y D TYA +W+IQ + D+D QL+EI+ D +
 35 Sbjct: 4045 AIPSLAANTLTIIVPDKSVYDQVVDNVYVYAGNVWQIQTIQSDGTNKQLNEISDDCN- 4103
 Query: 363 NLAWPLIVTALRAN--SAVKLQNNELSPVALRQMSCAAGTTQTACTDDNALAYNNNSKGG 536
 WPL++ A R N SA LQNNEL P L+ +G QT T YNNNS G
 40 Sbjct: 4104 ---WPLVIIANRHNEVSATVLQNNELMPAKLKTQVNSGPDQTCNTPTQ--CYNNNSNNG 4158
 Query: 537 RFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPKVKYLYFIKA*TT*I 716
 + V A+LSD LK+ + K DG + EL+PPC+F KG K+KYLK+K T
 Sbjct: 4159 KIVYAILSDVDGLKYTRILKDDG-NFVVLLEDPCKFTVQDVKGKIKYLYFVKGCNTLA 4217
 45 Query: 717 EVWCWAV*LLQYVFR-----EMLQKYLPIQLCFPSVLLQ*TLKHIKDYLASGGQPI 878
 W V + RL E + LC SV + T L D++ GG PI
 Sbjct: 4218 R--GWVVGTTISSTVRLQAGTATEYASNSSILSLCAFSVDPKKTLYL----DFIQGGTPIA 4271
 Query: 879 NCVKMLCTHTGTGQAITVTPEANMDQESXGGASCCLYCRCHIDHPNPKGXCDLKGKVVQI 1058
 NCVKMLC H GTG AITV P+A +Q+S GGAS C+YCR ++HP+ G C L+GK+VQ+
 50 Sbjct: 4272 NCVKMLCDHAGTGMAITVKPDATTNQDSYGGASVCIYCRARVEHPDVGDLCKLRGRFVQV 4331
 Query: 1059 PTTCANDPVGFTRLNRTVCTVCGMWKGYGCSCDQLREPLMQSADASKFLNGFAV 1217
 P DPV + L + VC VCG W+ CSC + +QS D + FLNGF V
 55 Sbjct: 4332 PVG-IKDPVSIVLTHDVCQVCGFWRDGS CSCVS-TDTTVQSKDTN-FLNGFGV 4381

Alignment 2 of translation 2 sequence

RNA-directed RNA polymerase (ORF1B) [murine hepatitis virus]

Identities = 24/44 (54%),

Query: 1199 FKRVCVSA-ARLTFCGTGTSTDVVYRAFDIYNEKVAGXAKFLK 1327
 FKR V G S ARL PC +G TDV RAFDI N AG + K
 65 Sbjct: 18 FKRVRGTSVNARLVPCASGLDQVQLRAFDICNANRAGIGLYYK 61

Fig. 2. Cont.

GAUUAUUUAUUAACAAUUCUACUAAUGUUGUUAUACGAGCAUGUAAACUUUGAAUUGUGUGACAACCCUUUCUUU
 GCUGUUUCUAAACCCAUGGGUACACAGACACAUACUAGAUAUUCGAUAAUGCAUUUAAUUGCACUUUCGAGU
 ACAUAUCUGAUGCCUUUUCGCUUGAUGUUUCAGAAAAGUCAGGUAAUUUUAAACACUUACGAGAGUUUGUGUU
 UAAAAUAAAGAUGGGUUUCUCUAUGUUUAUAAAGGGCUAUAACCUUAUAGAUGUAGUUCGUGAUCUACCUUCU
 5 GGUUUUAACACUUUGAAACCUAUUUUUAAAGUUGCCUCUUGGUUAUUAACAUUACAAUUUUAGAGCCAUUCUUA
 CAGCCUUUUCACCUGCUCAAGACAUUUGGGGCACGUCAGCUGCAGCCUAUUUUGUUGGCUAUUUAAAGCCAAC
 UACAUUUUAUGCUCUAGUAUGAUGAAAUGGUACAAUCACAGAUGCUGUUGAUUGUUCUCAAUUCACUUGCU
 GAACUCAAAUGCUCUGUUAAGAGCUUUGAGAUUGACAAAGGAAUUUACCAGACCUCUAAUUUCAGGGUUGUUC
 10 CCUCAGGAGAUGUUGUGAGAUUCCCUAAUUAUACAAACUUGUGUCCUUUUGGAGAGGUUUUUAAUGCUACUAA
 AUUCCCUUCUGUCUAUGCAUGGGAGAGAAAAAAUUUCUAAUUGUGUUGCUAUUACUCUGUGCUCUACAAC
 UCAACAUUUUUUUAACCUUUUAAGUGCUAUGGCGUUUCUGCCACUAAGUUGAAUGAUCUUUGCUUCUCCAAUG
 UCUAUGCAGAUUCUUUUGUAGUCAAGGGAGAUGAUGUAAGACAAUAGCGCCAGGACAAACUGGUGUUAUUGC
 UGAUUUAUAAUUAUAAUUGCCAGAUAUUUCAUGGGUUGUGUCCUUGCUUGGAUACUAGGAACAUUGAUGCU
 ACUUCACACUGGUAAUUAUAAUUAUAAUUAUAGGUUAUCUUGACAUGGCAAGCUUAGGCCCUUUGAGAGAGACA
 15 UAUCUAAUGUGCCUUUCUCCCGAUGGCAACCUUGCACCCACCUGCUCUAAUUGUUAUUGGCCAUUAAA
 UGAUUUAUGGUUUUUAACACCACUACUGGCAUUGGCUACCAACCUUACAGAGUUGUAGUACUUUUUUUGAACUU
 UUAUUAUGCACCGGCCACGGUUUGUGGACCAAAUUAUCCAUGACCUUUAUUAAGAACCAGUGUGUCAUUUUUA
 AUUUUAUUGGACUCACUGGUACUGGUGUGUUAACUCCUUCUUCAAAGAGAUUUAACCAUUUAACAAUUUGG
 CCGUGAUGUUUCUGAUUUCACUGAUUCCGUUCGAGAUCCUAAAACAUUCUGAAUUAUAGACAUUUCACCUUGC
 20 UCUUUUGGGGGUGUAAGUGUAAUUAACACUGGAACAAUUGCUUACUUGAAGUUGCUGUUCUUAUUAACAAGAU
 UUAACUGCACUGAUGUUUCUACAGCAAAUUCACUGCAGUACACUACACAGCUGGCGCAUUAUUAUUCUACUGG
 AAACAUGUAUUCAGACUCAAGCAGGCUGUCUUAUAGGAGCUGAGCAUGUCGACACUUCUUAUGAGUGCGAC
 AUUCCUAUUGGAGCUGGCAUUGUGCUAGUUAACAUACAGUUUCUUUAUUAACGUAGUACUAGCCAAAAUUCUA
 UUGUGGCUUAUACUAGUCUUUAGGUGCUGAUAGUUCAAUUGCUUACUCUAAUUAACCAUUGCUAUACCUAC
 25 UAACUUUUAUUAUGCAUUAUACAGAAUGCCUGUUUCUUAUGGCUAAAACCUCGUGAGAUUGUAAUUAUG
 UACAUCUGCGGAGAUUCUACUGAAUGUGCUAAUUGCUUCCCAAUAGGUAGCUUUUGCACACAACUAAUUC
 GUGCACUCUCUGGUUAUUGCUGCUGAACAGGAUCGCAACACAC

Translation 1

30 Nucleotides 3 to 818: Frame 3 272 aa (orf lab)
 LQNYGENAVIPQGIMMNVAKYTQLCQYLNTLT LAVPYNMNRVIHFGAGSDKGVAPGTAVLRQWLPTGTLTLLVDSLDNDFVSDA
 DSTLIGDCATVHTANKWDLIISDMYDPRTKHVTENDSKGFFTYLCGFIKQKLALGGSIAVKITEHSWNADLYKLMGHFS
 WWTAFVTNVNASSSEAFLLIGANYLGKPKQIDGYTMHANYIFWRNTNPIQLSSYSLFDMSEKFLPLKRGTAVMSLKENQIND
 35 MIYSLLEKGRLLIRENNRVVSSDILVNN

Translation 2

40 Nucleotide 828 to 3089: Frame 3 756 aa (S protein)
 MFIFLLFLTTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFLFPFYSNVTGFHTINHTFGNPVI
 PFKDGIFYAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVIRACNFELCDNPFPAVSKPMGTQHTMI FDNFNCTFE
 YISDAFSLDVSEKSGNFKHLREFVFNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSPAQD
 45 IWGTSAAAYFVGYLKPTTFMLKYDENGTTDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPFGDVVRFPNITNLCP
 FGEVFNATKFPFSVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGGDDVRQIAPGQTGVI
 ADYNYKLDPDDFMGCLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKCTPPALNCWPLNDYGEYTT
 TGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFENGLTGTGVLTPSSKRFQPFQFGRDVSDFDTSVRDPKT
 SEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTAQGLIGAHEVDTSYEC
 50 DIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMICYGDS
 ECANLLLQYGSFCTQLNRALSWYCC

Alignment 1 of translation 1

55 replicase [bovine coronavirus]
 Identities = 183/271 (67%),

Query: 3 LQNYGENAVIPQGIMMNVAKYTQLCQYLNTLT LAVPYNMNRVIHFGAGSDKGVAPGTAVLR 182
 L NYG+ +P G MMNVAKYTQLCQYLNT TLAVP NMRV+H GAGS+KGVAPG+AVLR
 60 Sbjct: 6822 LWNYGKPVTLPTGCMNNVAKYTQLCQYLNTTTLAVPVNMRVLHLGAGSEKGVAPGSAVLR 6881
 Query: 183 QWLPTGTLTLLVDSLDNDFVSDADSTLIGDCATVHTANKWDLIISDMYDPRTKHVTENDSK 362
 QWLP GT+LVD+DL FVSD+ +T GDC T+ +WDLIISDMYDP TK++ + N SK
 65 Sbjct: 6882 QWLPAGTILVDNDLYPFVSDSVATYFGDCITLFPDCQWDLIISDMYDPITKNIGEYNVSK 6941
 Query: 363 EGFFTYLCGFIKQKLALGGSIAVKITEHSWNADLYKLMGHFSWWTAFVTNVNASSSEAF 542
 +GFFTY+C I+ KLALGGS+A+KITE SWNA+LYKLMG+F++WT F TN NASSSE FL

Fig. 2. Cont.

Sbjct: 6942 DGFFTYICHMIRDKALGGSSVAIKITEFSWNAELYKLMGYFAFWTVFCTNANASSSEGFL 7001

Query: 543 IGANYLGKPKKEQIDGYTMHANYIFWRNTNPIQLSSYSLFDMSEKFKPLKRGTAVMMLKENQ 722

5 Sbjct: 7002 IG NYLGKPK +IDG MHANY+FWRN+ +YSLFDM+KFPLKL GTAV++L+ +Q
IGINYLGKPKVEIDGNVMHANYLFWRNSTVWNGGAYSLFDMKFKPLKLAGTAVINLRADQ 7061

Query: 723 INDMIYSLLEKGRLLIIRENNRVVSSDILVN 815

INDM+YSLLEKG+L++R+ N+ V D LVN

Sbjct: 7062 INDMVYSLLEKGRLLVRDNTNKEVFGVDSLVD 7092

10

Alignment 2 (Spike protein of coronavirus)

E2 glycoprotein precursor - murine hepatitis virus (strain JHM); contains spike glycoprotein

15 Identities = 199/798 (24%), Positives = 314/798 (39%), Gaps = 48/798 (6%)
Frame = +3

Query: 828 MFIFLLFLTLTSGSDLDRCCTTFDDVQAPNYTQHTSSM-----RGVYYP-DEI 965
+F+F+L L G D F +Q NY + +S RG YY D +

20 Sbjct: 2 LEVFILLLLPSCGLYIGD----FRCIQTVNNGNNASAPSISTEAVDVSKGRGTYVLDLV 57

Query: 966 FRSDTLTYLTQDLFLPF----YSNV--TGFTHTINHTFGNP--VIPFKDGIYFAATE-KSNV 1118
+ + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N

25 Sbjct: 58 YLNATLLLTG--YYPVDGNSYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKVQNLKTNT 115

Query: 1119 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFELCDNPFPAVSKPMGTQHT 1277
G V GS N C + +C P+ KP

Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTICQLPY-TPCKP----- 167

30 Query: 1278 MIFDNAFNCTFEYISDAFSLDVSEKSGNEFKHLREFVFKNKDGFLYVY---KGYQPIDVVR 1448

N + + DV K R F F +LY + +G

Sbjct: 168 -----NTNGNRVIGFWHTDVKKPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218

35 Query: 1449 DLPSGFNTLKPIFKPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYD 1628
D PS L F + +G +T + + +P T A Y+V L ++ ++

Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPICTPTAG--STLAPLYWVTPLLKRQYLFNFN 273

Query: 1629 ENGTITDAVDCSQNPLAELKCSVKSEIDKGIYQTSNFRVPSGDVVR-FPNITNLCFPG 1805
E G IT AVDC+ + +E+KC +S G+Y S + V P G V R PN+ + C

40 Sbjct: 274 EKGVITSADVDCASSYISEIKCKTQSLPSTGVYDLGTYVQPVGVVYRRVNPPLD-CKIE 332

Query: 1806 EVFNATKFPSVYAWERKKISNCVADYSLYNSTFFSTFKCYGVSATKLNLCFSNVYADS 1985
E A PS WER+ NC + S L + C + A+K+ +CF +V D

45 Sbjct: 333 EWLTAKSVPSPNLWERRTFQNCNENLSSLLRYVQAESLSCNNIDASKVYGMCFGVSVDK 392

Query: 1986 FVVKGDVVRQIAPGQTGVADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHG 2165
F + + G +G + NYK+ C L ++ + T NYN R+G

Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVT-INNNPSSWNRRY 451

50 Query: 2166 KLRPFERDISNVFSPDGKPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFELLNA 2345

+ +ND R + + LLN

Sbjct: 452 -----FKVND-----RCQIFANILLNG 468

55 Query: 2346 --PATVCGPKL---STDLIKQCVNFNFGLTGTGVLTLP-SSKRFQPFQFGRDVSDFTD 2507
T C L +T++ CV ++ G+TG GV + + +Q DV+ +

Sbjct: 469 INSGTTCSTDQLPNTTEVATGVCVRYDLYGITGQGVFKEVKADYNSWQALLYDVNGNLN 528

Query: 2508 SVRDPKTSEILDISPCSGFVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWR 2687
RD T++ I C G VS + E A+LY+++NC+ V T + + P

60 Sbjct: 529 GFRDLTNTKTYTIRSCYSGRVSAAY--HKEAPEPALLYRNINCSYVFTNNISREENPL-- 584

Query: 2688 IYSTGNNVFQTOAGCLIGAEH--VDTSYECDIPIGAGICASYHTVSLR---STSQK--S 2846
N F + GC++ A++ + C++ +GAG+C Y R ST + +

65 Sbjct: 585 -----NYFDSYLGCVVNADNRTDEALPNCNLRMGAGLCVDYSKRRARRSVSTGYRLTT 638

Query: 2847 IVAYTMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMKTSVDCNMICYDSTECA 3023
Y L DS + + IPTNF+I E + + K ++DC ++CGD+ C

Sbjct: 639 FEPYMPMLVNDVSVQSVGGLEYMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACR 698

70 Query: 3024 NLLLQYGSFCTQLNRALS 3077

Fig. 2. Cont.

L++YGSFC +N L+
 Sbjct: 699 QQLVEYGSFCDNVNAILN 716

RDG1 seq

5 UUCAAGGCcUUCAAACNUAUGUAACACAACAACUAAUCAGGGMUGcUGAAAUCHCGSCUUCUGCUAAUCUUGC
 UGCUACUAAAAUGUCUGAGUGUGUUCUUGGACAAUCAAAGAGUUGACUUUUGUGGAAAGGGCUACCACCUU
 AUGUCCUCCCACAAGCAGCCCCGCAUGGUGUUGUCUCCUACAUGUCACGUAUGUGCCAUCCCAGGAGAGGA
 10 ACUUCACCACAGCGCCAGCAAUUUGUCAUGAAGGCAAAGCAUACUCCUCGUGAAGGUGUUUUUGUGUUUAA
 UGGCACUUCUUGGUUUUAUUACACAGAGGAACUUCUUUUCUCCACAAAUAUUACUACAGACAAUACAUUGUC
 UCAGGAAAUUGUGAUGUCGUUAUUGGCAUCAUUAACAACACAGUUUAUGAUCCUCUGCAACCUGAGCUUGACU
 CAUUCAAAGAAGAGCUGGACAAGUACUUCAAAAUCAUACAUCACCAGAUGUUGAUCUUGGCGACAUUUCAGG
 CAUUAACGCUUCUGUCGUCAACAUAUCAAAGAAAUUGACCGCCUCAUGAGGUGCGUAAAAUUUAAUGAA
 UCACUCAUUGACCUUCAAGAAUUGGGAAAAUAUGAGCAAUAUAUUAAGUGgCCCUGGUACGUCUGGGU

Translation 1

Nucleotides 3 to 650: Frame 3; 216 aa

QSLQXYVTQQLIRXAEIXXSANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAIC
 20 HEGKAYFPREGVVFENGTSWFITQRNFFSPQIITDNTFVSGNCDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPD
 VDLGDISGINASVNNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVW

Translation 2

Nucleotides 37 to 339: Frame 1; 101 aa

SGXLKXXLLLILLKLSVFLDNQKELTFVERATTLCPSHKQPRMVLSSYMSRMCHPRRGTSPPQRQQFVMKAKHTSLVKV
 25 FLCMLALLGLLHGRGTSFLHK

Translation 3

Nucleotides 343 to 576: Frame 1; 78 aa

LLQTIHLSQEIVMSLLASLTTFMILCNLSLTHSKSWTSTSKIHHQMLLILATFQALTLLSSTFKKLTASMRSLKI
 30

Alignment of translation 1

S glycoprotein [murine hepatitis virus]
 Length = 1376

35 Identities = 86/218 (39%), Positives = 129/218 (59%), Gaps = 3/218 (1%)
 Frame = +3

Query: 6 SLQTYVTQQLIRXAEIXXSANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVF 185
 +L Y+++QL I SA A K++ECV Q+ R++FCG G H++S Q AP+G+ F
 40 Sbjct: 1105 ALNAYISKQLSDSTLIKFSAAQAIEKVNCEVKSQTTRINFCGNGNHILSLVQNAPYGLYF 1164

Query: 186 LHVITYVPSQERNFTTAPAICHEG-KAYFPREGVVFENGTSWFITQRNFFSPQIITDNTF 362
 +H +YVP+ +P +C G + P+ G FV + W T +++ P+ IT N+
 45 Sbjct: 1165 IHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFSGSSYYYPEPITDKNSV 1224

Query: 363 VSGNCDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDISGINASVNNI 536
 V +C V +P + L FKEELDK+FKN TS PD+ L D +N + +++
 Sbjct: 1225 VMSSCSVNYTKAPEVLLNSSIPNLPDFKEELDKWFKNQTSIAPDLSL-DFEKLNVTFDL 1283

50 Query: 537 QKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVW 650
 E++R+ E K LNES I+L+E+G YE Y+KWPWYVW
 Sbjct: 1284 SDEMNRIQEAIKKLNESEYINLKEVGTYEMYVKWPWYVW 1321

EMC-8

AGGCCAAAACAGCGCCGACCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUACACAGCUCUCACUCAGCAUG
 GCAAGGAGGAACUUAGAUAUCCUCGAGGCCAGGGCGUCCAUAACACCAAUAGUGGUCCAGAUGACCAAAU
 UGGCUACUACCGAAGAGCUACCCGACGAGUUCGUGGUGGUGACGGCAAAUUGAAAGAGCUCAGCCCCAGAUGG
 60 UACUUCUAUUACCUAGGAACUGGCCCCAGAAGCUUCACUCCCUACGGCGCUAACAAGAAGGCAUCGUUAGGG
 UUGCAACUGAGGGAGCCUUGAAUACACCCAAAGACCACAUUGGCACCCGCAAUCCUAAUAAUAAUGUUGCC

Translation

Nucleotides 1 to 363: Frame 1; 121 aa

RPKQRRPQGLPNNTASWFTALTQHGKEELRFRGQGVPIINTNSGPDQIGYRRATRRVRGGDGKMKELSPRWYFYLLGTG
 65 PEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNXA

Fig. 2. Cont.

Alignment

nucleocapsid protein - bovine coronavirus (strain Mebus)

5 Identities = 55/129 (42%),

Query: 1 RPKQRRPQGLPNNTA-----SWFTALTQHGK-EELAFPRGQGVPIINTNSGPDQIGYYRR 162

+PKQ LP+ SWF+ +TQ K +E F GQGVPI + GY+ R

10 Sbjct: 44 QPKQTATSQLPSGGNVVPYYSWFSGITQFQKGKEFEFAEGQGVPIAPGVPATEARGYWYR 103

Query: 163 ATRR-VRGGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVVWATEGA-LNTPKDHIG 336

RR + DG ++L PRWYFYLLGTGP A YG + +G+ WVA+ A +NTP D I

Sbjct: 104 HNRRSFKTADGNQRQLLPRWYFYLLGTGPHAKDQYCTDIDGVFVWASNQADVNTPAD-IL 162

15 Query: 337 TRNPNNNXA 363

R+P+++ A

Sbjct: 163 DRDPSSDEA 171

EMC-11: unknown sequence

20 UUGCAUACCGCAAUGUUCUUCUUCGUAAGAACGGUaAUAAGGGAGCCGGUGGUCAUAGCUgUGGCAUGAUCUA
 AAGUCUUAUGACUUAAGGUGACGAGCUUGGCACUGAUCCCAUUGAAGAUUAUGAACAAAACUGGAACACUAAGC
 AUGGCAGUGGGUGACUCCGUGAACUCACUCGUGAGCUCUAUGGAGGUGCAGUCACUCGCUAUGUCGACAACAA
 UUUCUGUGGCCAGAUUGAUUACAUCGAGUCGaAGAGAGGUGUCUACUGCUGCCGUGACCAUGAGCAUGAAAA
 ACUCUUUCCGAACAACUUGAUUACAUCGAGUCGaAGAGAGGUGUCUACUGCUGCCGUGACCAUGAGCAUGAAAA
 25 UUGCCUgGGUUCACUGAGCGCUCUGAUAAAGAGCUACGAGCACCAGACACCCUUCGaAAUUAAGAGUGCCAAGA
 AAaUUGACACUUAUCAAAGGGGAAUGCCCCAAAGCUUGUGUUUCCUCUUAACUCAAAGUCAAGUCAUUCAA
 CCACGUGUUGAAAAGAAAAAGACUGAGGGUUUCAUGGGGCGUAUACGCUCUGUGUACCCUGUUGCAUCUCCAC
 AGGAGUGUAACAAUAGCACUUGUCUACCUUGAUGAAUGUAUUAUUGCGAUGAAGCUUCAUGGCAGACGUG
 CGACUUUCUGAAAGCCACUUGUGAACAUUGUGGCACUGAAAUAUUAGUUAUUGAAGGACCUAGUACAUGUGGG
 30 UACCUACCUACUAAUGCUGUAGUGAAAAUGCCAUGUCCUGCCUGUCAAGACCCAGAGAUUGGACCUGAGCAUA
 GUGUUGCAGAUUAUACACAACCACUCAAAAUUGAAACUCGACUCCGCAAGGGAGGUAGGACUAGAUGUUUUGG
 AGGCUGUGUGUUUGCCUAUGUUGGCUGCUAAUAUAGCGUGCCUACUGGGUUCUCCUGUGCUAGUGCUGAUUU
 GGCUCAGGCCAUACUGGCAUUAACUGGUGACAAUGUGGAGACCUUGAAUGAGGAUCUCCUUGAGAUACUGAGUC
 GUGAACGUGUUAACAUUAACAUUGUUGGCGAUUUUCAUUUGAUGAAGAGGUUGCCAUCAYUUUGGCAUCYUU
 35 CUCUGCUUCUACAAGUGCCUUUAUUGACACUAUAAAGAGUCUUGAUAACAAGUCUUUCAAACCAUUGUUGAG
 UCCUGCGGUAACUAUAAAGUUACCAAGGGAAAGCCCGUAAAAGGUGCUUGGAACAUGGACAACAGAGAUACAG
 UUUUAACACCACUGUGUGGUUUUCCUCACAGGCUGCUGGUGUUAUCAGAUCAAUUUUUGCGCGCACACUUGA
 UGCAGCAAACCACUCAAUUCCUGAUUUUGCAAAGAGCAGCUGUCACCAUACUUGAUGGUUAUUUCUGAACAGUCA
 UUACGUCUUGUCGACGCCAUGGUUUUAUACUUCAGACCUGCUCACCAACAGUGUCAUUAUUAUGGCAUAUGUAA
 40 CUGGUGGUCUUGUACAACAGACU

Translation of putative open reading frames

45 >~out: 78 to 1: Frame -2 26 aa
 DFRSCHSYDHRLPYYRSYEEHCGMQ
 >~out: 59 to 379: Frame 2 107 aa
 LWHDLKSYDLGDELGTDPIEDYEQNWNTHKSGALRELTREINGAVTRYVDNNFCGPDGYPLDCIKDFLARAGKSMCTLS
 EQLDYIESKRGVYCCRDHEHEIAWVH
 50 >~out: 283 to 89: Frame -1 65 aa
 LARACEKIFDAIKRVPWATEIIVVDIASDCTSIELTSEFTECTAMLSVPVLFIIIFNGISAKLVT
 >~out: 90 to 614: Frame 3 175 aa
 VTSALALIPLKIMNKTGTLMAVVHVSNSLVSSMEVQSLAMSTTISVAQMGTLIIASKIFSHARASQCALFPNNLITSSRRE
 VSTAAVTMSMKLPGFTERS DKSIEHQTPFEIKSAKKIDTFKRGMPQSLCFLLTQKSKSFNHVLKRRLRVSWGVYALCTLL
 55 HLHRSVTICTLP
 >~out: 204 to 124: Frame -2 27 aa
 RVTAPPLSSRVSSRSAPLPCLVFQFCS
 >~out: 312 to 208: Frame -2 35 aa
 SSCSERVHIDLPARARKSLMQSRGYPSGPQKLLST
 60 >~out: 485 to 258: Frame -3 76 aa
 EETQALGHSPFESVNFGLTLNFEGLVLVALIRALSEPRQFHAHGHGSSRHLSSTRCNQVVRKECTLTCPRVREN
 >~out: 397 to 287: Frame -1 37 aa
 LLSERSVNPNGFMLMVTAAVDTSRLDVIKLFKSAH
 >~out: 364 to 486: Frame 1 41 aa
 65 NCLGSLALIRATSTRHPSKLRVPRKLTLSKGECPKACVSS
 >~out: 490 to 401: Frame -1 30 aa
 VKRKHLWGIPLLVKVSIFLALLISKGVWCS
 >~out: 446 to 1483: Frame 2 346 aa

EMC12: unknown sequence .

Translation of putative open reading frames

```

55 >~out: 3 to 446: Frame 3 148 aa
LAHAETRKLMPICMVRAIMATIQRKYKGIKIQEGIVDYGVRFFFFYTSKEPVASIITKLNSLINEPLVTMPIGYVTHGFNL
EEAARCMRSLKAPAVSVSSPDAVTTYNGYLTSSSKTSEEHFVETVSLAGSYRDWSYSGQRTTELGE
>~out: 100 to 11: Frame -2 30 aa
ILIPLYLRWMVAIMALTSMHIGINFLVSSA
>~out: 188 to 33: Frame -1 52 aa
RVQLRNNRSYRLFTSIKEESDTIVNDALLNFNSFILTLDGCHYGSNIHAYRH
60 >~out: 64 to 159: Frame 1 32 aa
WQPSNVSIKELKFKRASLTMVSDSSFILVKSL
>~out: 220 to 143: Frame -2 26 aa
PIGIVTSGSFREFSFVIEATGSLLV
>~out: 293 to 192: Frame -1 34 aa
65 HYGRSFKRTHHTARSLFKIKTMCHITNWHCDKRLI
>~out: 397 to 224: Frame -2 58 aa
EPAKETVSTKCSSDVFDEVRYPYVVTASGDDTDTTAGALRERIQRASSRLKPCVT
>~out: 229 to 288: Frame 1 20 aa

```

Fig. 2. Cont.

```

      HMLVILKRLRAVCVLLKLLP
      >~out: 292 to 372: Frame 1      27 aa
      CQYHHQMLLLHIMDTSLRHQRHLRSTL
      >~out: 444 to 340: Frame -3     35 aa
5     QHLTLYAVLNRTNLCKSQPKKLFQSAPQMSLMTK
      >~out: 416 to 351: Frame -1     22 aa
      IGPISVRASQRNCFYKVLLRCL
      >~out: 365 to 445: Frame 2      27 aa
      GALCRNSFFGWLLQRLVLFRTAYRVRC
10    >~out: 376 to 435: Frame 1     20 aa
      KQFLWLALTEIGPIQDSVQS
```

15

Figure 3.

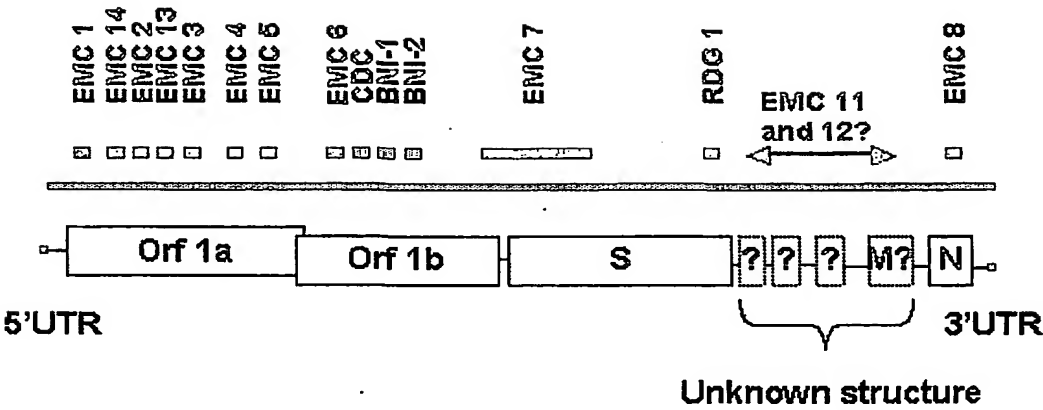


Figure 4.

Comparison of N-termini of the S proteins of the group 2 coronaviruses

5

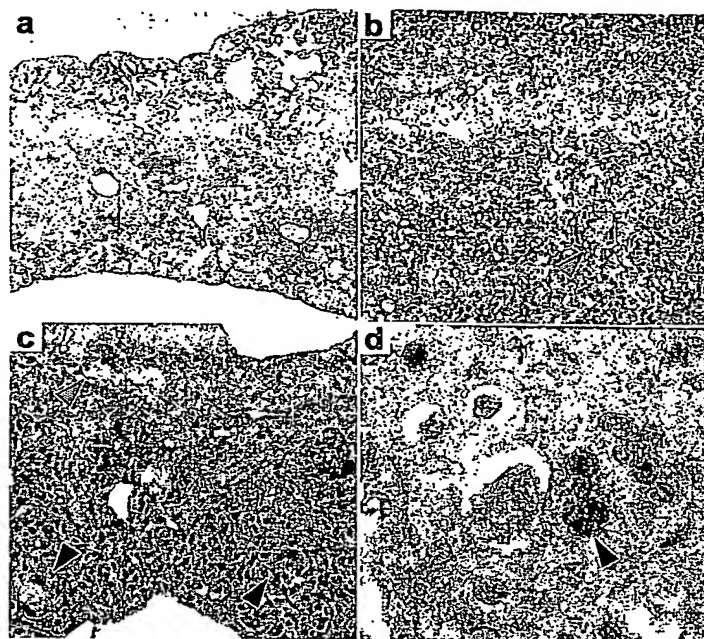
HCV OC43	MFLILLISLPTAFAVIGDL- KCTTVS INDID
MHV A59	MLFVFILFLPSCLGIGDF- RCIQLVNS NGA
BCV	MFLILLISLPMFAFAVIGDL- KCTTVS INDVD
SARS	MF-IFLLFL-TLTSG-SDLDRCTTFDDVQAP

10

Figure 5.



Figure 6.



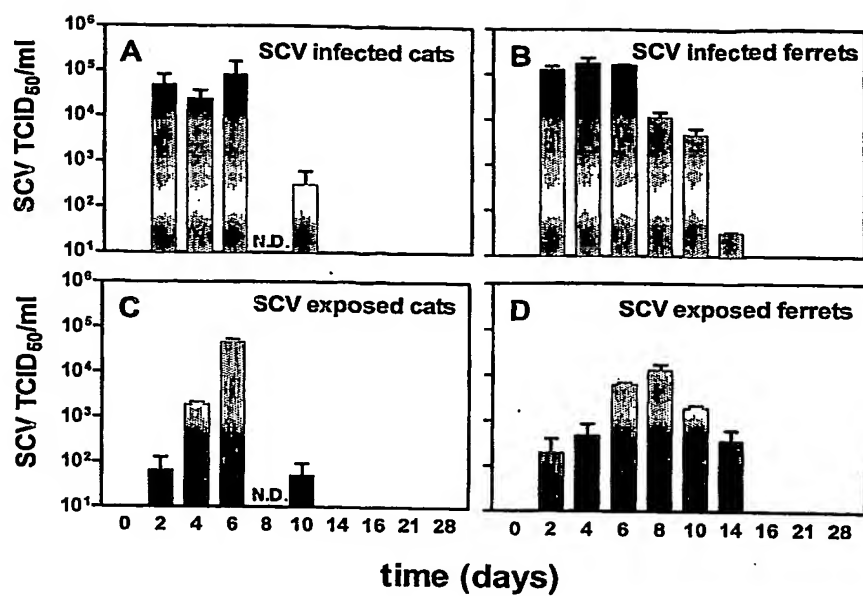


Figure 7.

Figure 8 Detection of SCV in postmortem tissues of experimentally SCV infected cats and ferrets

Tissue	Cats				Ferrets			
	1	2	3	4	1	2	3 [†]	4
Trachea	+/	+/	+/	+/	+/	+/	+/	+/
	+*	+	+	+	+	+	+	+
Lung	+/	+/	+/	+/	+/	+/	+/	+/
	+	+	+	+	+	+	+	+
Tracheo-bronchial lymph node	-/-	+/	+/	-/-	+/	+/	+/	+/
Duodenum	-/-	-/-	+	+/	+	+	+	-/-
	-	-	-	+	-	+	-	-
Jejunum	-/-	-/-	-/-	-/-	-/-	-/-	+/	-/-
	+	+	+	+	+	+	+	+
Ileum	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
	+	+	+	+	+	+	+	+
Mesenteric lymph node	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
	+	+	+	+	+	+	+	+
Kidney	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
	+	+	+	+	+	+	+	+
Urinary bladder	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
	+	+	+	+	+	+	+	+
Peripheral blood mononuclear cells	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
	+	+	+	+	+	+	+	+

* virus isolation/real time PCR results are depicted at day 4 p.i.

[†] died during the experiment.

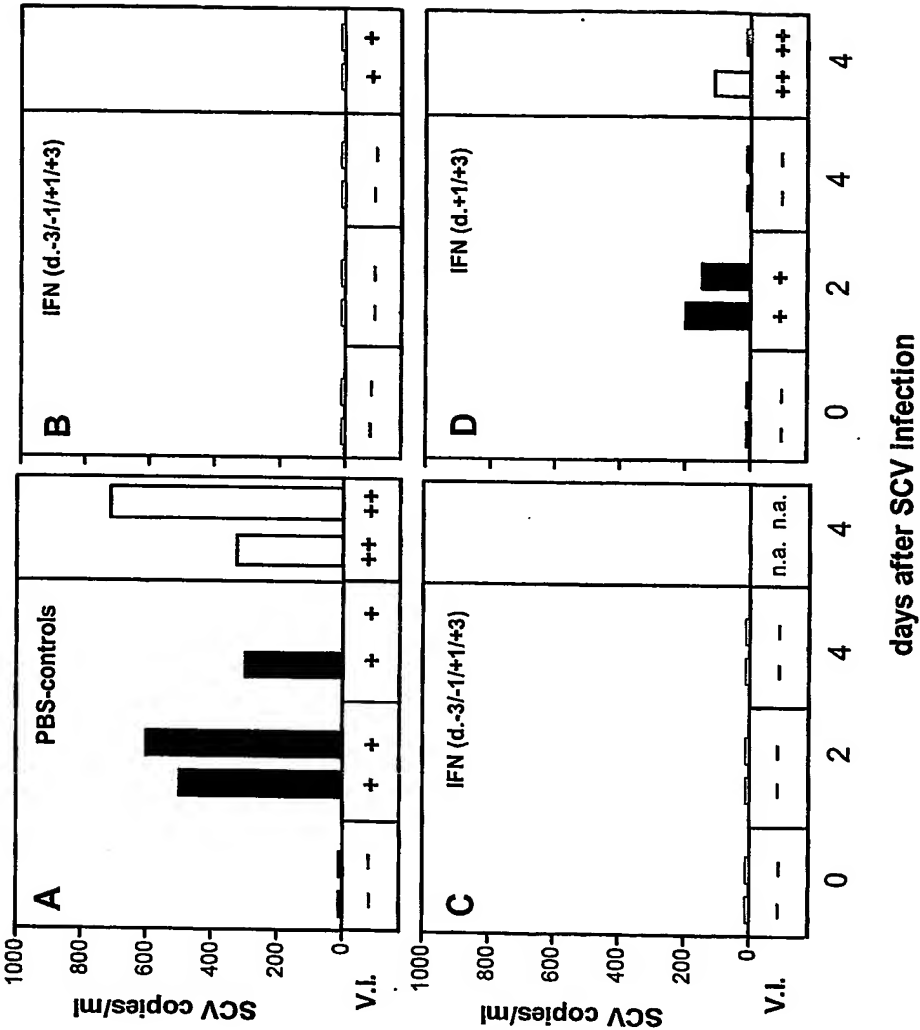


Figure 9

Figure 10

1 atattaggtt tttaacctacc caggaaaaagc caaccaacct cgatctcttg tagatctgtt
 61 ctctaaacga actttaaat ctgtgtagct gtgcctcgcc tgcataccta gtgcacctac
 121 gcagtataaa caataataaa ttttactgtc gttgacaaga aacgagtaac tcgtccctct
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Fig. 10. Cont

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig 10. Cont.

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Fig 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

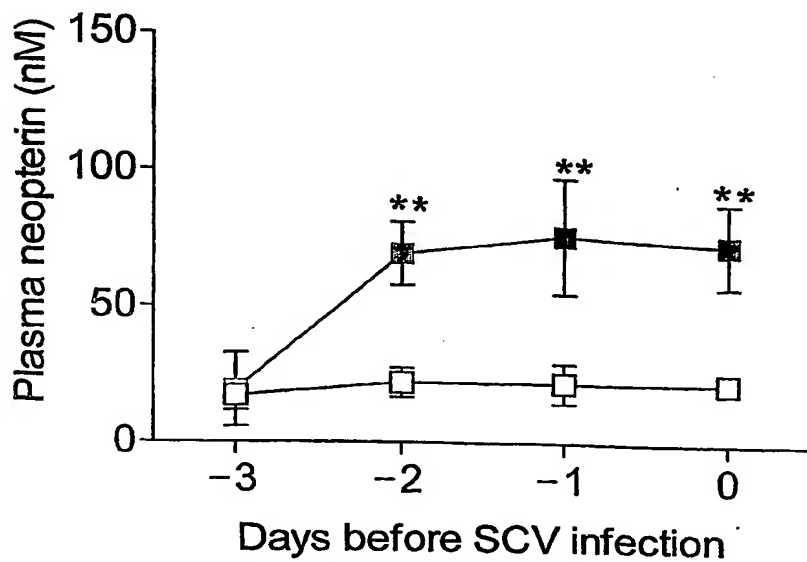
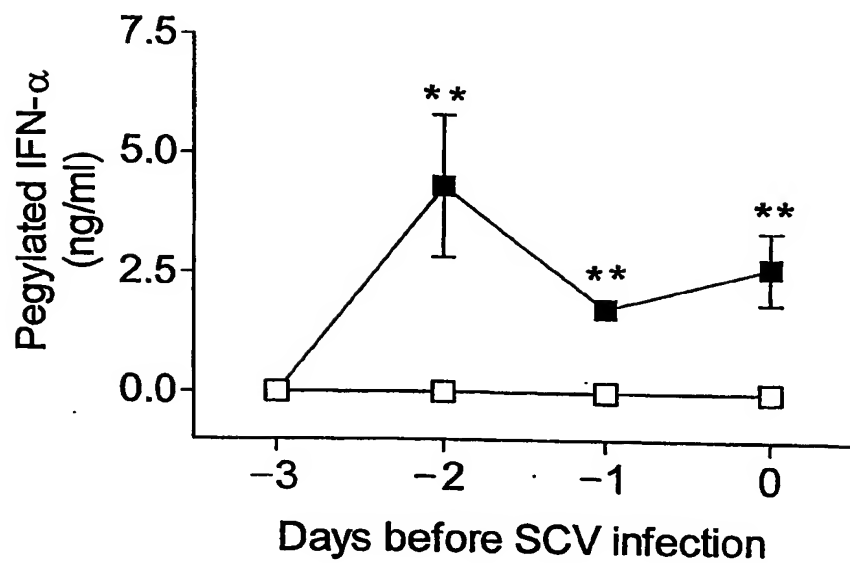
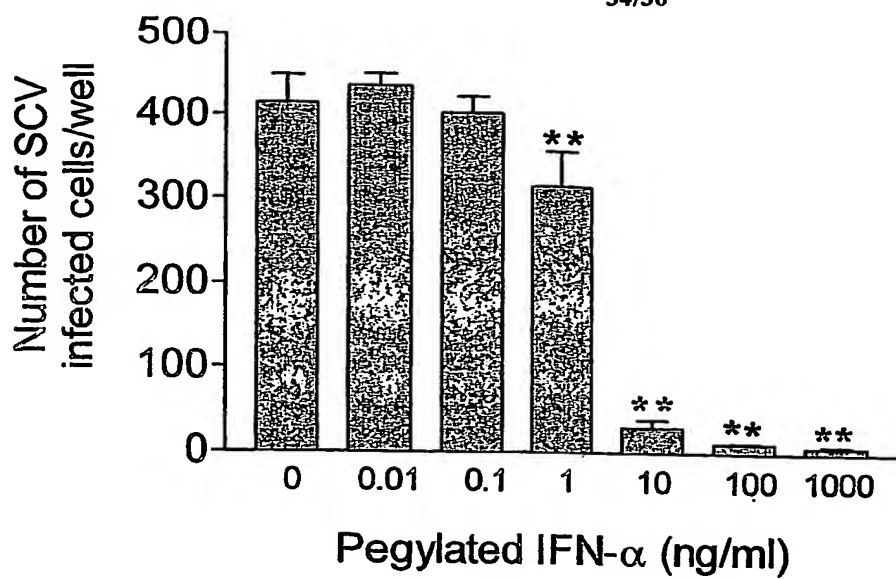
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 27001 aactataaat taaatacaga ccacgccggt agcaacgaca atattgcttt gctagtacag
 27061 taagtacaa cagatgtttc atctgttga ctccaggtt acaatagcag agatattgat
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 27181 agtgagacaa ttatttaagc ctctaactaa gaagaattat tcggagttag atgatgaaga
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 27301 ttgtatttac atcttgagcag ctatatcact atcaggagtg tgttagaggt acgactgtac
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 27541 aagaggaggt tcaacaagag ctctactcgc cactttttct cattgttgcg gctctagtat
 27601 tttaataact ttgcttcacc attaaagaa agacagaatg aatgagctca ctttaattga
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 27721 ttggttttca ctgaaaatcc aggatctaga agaacttgt accaaagtct aaacgaacat
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 27841 gcgctgtgca tctaataaac ctcatgtgct tgaagatcct tgtaagggtac aacactaggg
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 27961 ggcacactat ggttcaaaac tatagctagg tgttggctacc ttaccaaact gctgcattta
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 28801 ttgaaccagc ttgagagcaa agtttttggt aaaggccaa acaacaagg ccaactgtc
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 28921 cagtacaacg tcaactcagc atttggaga cgtggtccag acaaaaccca aggaatttc
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 29161 aaagacaacg tcatactgct gaacaagcac attgacgcat acaaacatt ccacacaaca
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Fig. 10. Cont.

29281 aagaagcagc ccactgtgac tcttcttctct gcggtgaca tggatgatt ctccagacaa
29341 cttcaaat ccatgagtgg agcttctgct gatccaactc aggcataaac actcatgatg
29401 accacacaag gcagatgggc tatgtaaacg ttttcgcaat tccgtttacg atacatagtc
29461 tactcttgtg cagaatgaat tctcgtaact aacacagcaca agtaggttta gttaaacttta
29521 atctcacata gcaatcttta atcaatgtgt aacattaggg aggacttgaa agagccacca
29581 catcttcacg gaggccacgc ggagtagcat cgaggggtaca gtgaataatg ctaggggagag
29641 ctgacctat ggaagagccc taatgtgtaa aattaatctt agtagtgcta tcccctgtg
29701 attttaatag ctctcttaga gaatgacaaa aaaaaaaaaa a

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Fig 11



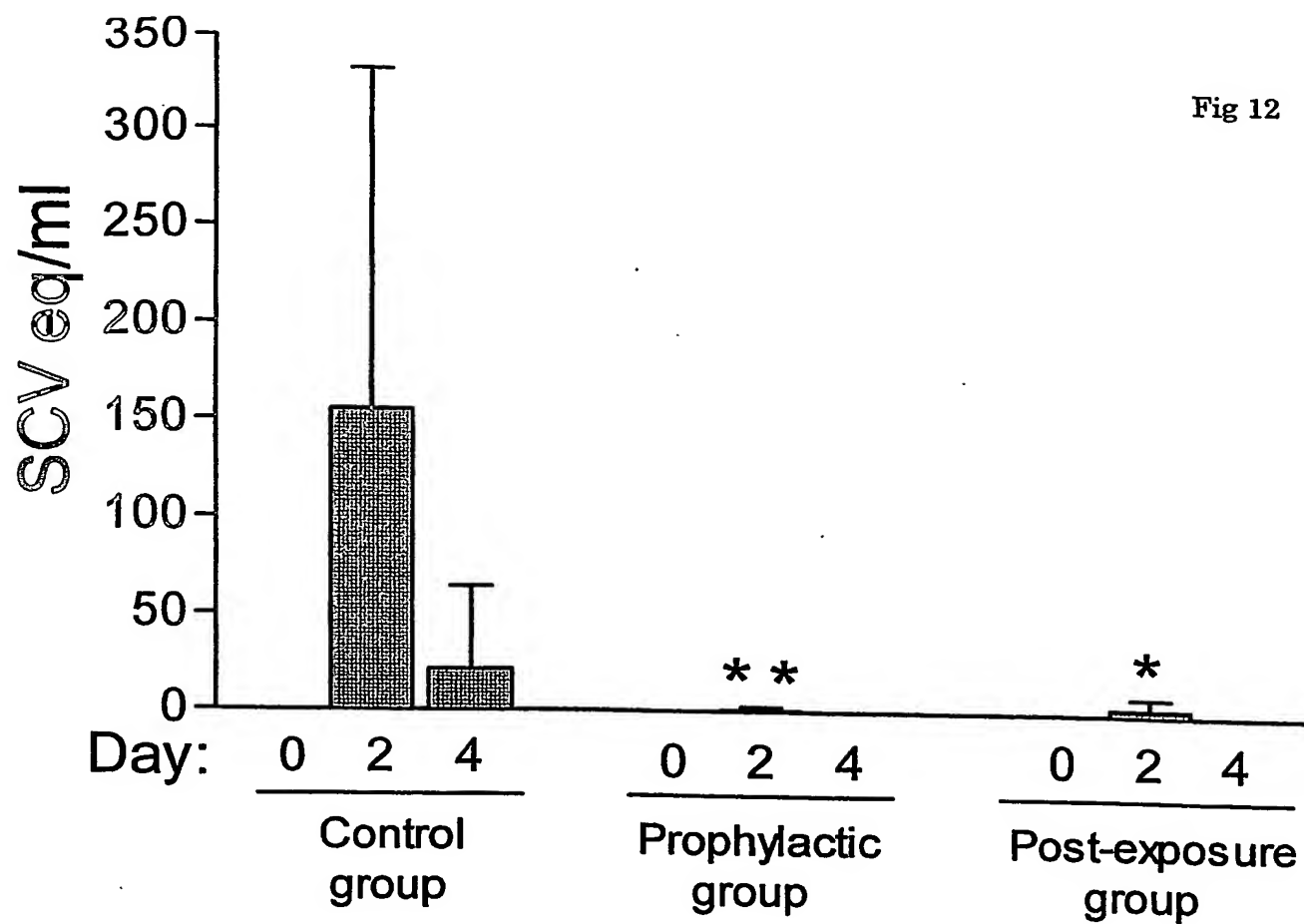


Fig 13

